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Val Asn Gly Thr	5	10		15
Gly Gln His Trp		25	30	-
Ile Gly Ile Thr		40	45	
Gln Ala Asp Val	55		60	
Phe His Gln Lys	70	•	75	80
Leu Gln Ser Ala	85	90		95
Gly Asp Val Val		105	110	_
Val Thr Ala Val 115	Glu Val Asp 1	Pro Ala Asp An 120	rg Asn Arg Val 125	Ile Ser

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Gly Glu His Arg Ile Lys Ala Trp Thr His Phe His Phe Pro Gly Arg
                         135
                                             140
Gly Ser Thr Tyr Ser Asp Phe Lys Trp His Trp Tyr His Phe Asp Gly
                     150
                                         155
Thr Asp Trp Asp Glu Ser Arg Lys Leu Asn Arg Ile Tyr Lys Phe Gln
                 165
                                     170
Gly Lys Ala Trp Asp Trp Glu Val Ser Asn Glu Asn Gly Asn Tyr Asp
             180
                                 185
Tyr Leu Met Tyr Ala Asp Ile Asp Tyr Asp His Pro Asp Val Ala Ala
                             200
                                                 205
Glu Ile Lys Arg Trp Gly Thr Trp Tyr Ala Asn Glu Leu Gln Leu Asp
                         215
                                             220
Gly Phe Arg Leu Asp Ala Val Lys His Ile Lys Phe Ser Phe Leu Arg
                     230
                                         235
Asp Trp Val Asn His Val Arg Glu Lys Thr Gly Lys Glu Met Phe Thr
                 245
                                     250
Val Ala Glu Tyr Trp Gln Asn Asp Leu Gly Ala Leu Glu Asn Tyr Leu
                                 265
Asn Lys Thr Asn Phe Asn His Ser Val Phe Asp Val Pro Leu His Tyr
                             280
                                                 285
Gln Phe His Ala Ala Ser Thr Gln Gly Gly Gly Tyr Asp Met Arg Lys
                         295
                                             300
Leu Leu Asn Ser Thr Val Val Ser Lys His Pro Leu Lys Ala Val Thr
                     310
                                         315
Phe Val Asp Asn His Asp Thr Gln Pro Gly Gln Ser Leu Glu Ser Thr
                                     330
Val Gln Thr Trp Phe Lys Pro Leu Ala Tyr Ala Phe Ile Leu Thr Arg
            340
                                 345
Glu Ser Gly Tyr Pro Gln Val Phe Tyr Gly Asp Met Tyr Gly Thr Lys
                             360
Gly Asp Ser Gln Arg Glu Ile Pro Ala Leu Lys His Lys Ile Glu Pro
                        375
Ile Leu Lys Ala Arg Lys Gln Tyr Ala Tyr Gly Ala Gln His Asp Tyr
                    390
                                         395
Phe Asp His His Asp Ile Val Gly Trp Thr Arg Glu Gly Asp Ser Ser
                405
                                     410
Val Ala Asn Ser Gly Leu Ala Ala Leu Ile Thr Asp Gly Pro Gly Gly
            420
                                425
                                                     430
Ala Lys Arg Met Tyr Val Gly Arg Gln Asn Ala Gly Glu Thr Trp His
        435
                            440
Asp Ile Thr Gly Asn Arg Ser Glu Pro Val Val Ile Asn Ser Glu Gly
                        455
                                            460
Trp Gly Glu Phe His Val Asn Gly Gly Ser Val Ser Ile Tyr Val Gln
465
                    470
                                        475
Arg
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<sup>&</sup>lt;210> 7

<sup>&</sup>lt;211> 1446

<sup>&</sup>lt;212> DNA

<sup>&</sup>lt;213> Künstliche Sequenz

<sup>&</sup>lt;220>

<sup>&</sup>lt;223> Beschreibung der künstlichen Sequenz: Fusion der Alpha-Amylas -Gene von B. licheniformis und B. amyloliquefaciens (AL76).

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gta aat ggc Val Asn Gly 1	acg ctg Thr Leu 5	atg cag ta Met Gln Ty	t ttt gaa r Phe Glu 10	Trp Tyr Th	g ccg aac gac r Pro Asn Asp 15	48
ggc cag cat Gly Gln His	tgg aaa Trp Lys 20	cga ttg ca Arg Leu Gli	g aat gat n Asn Asp 25	gcg gaa cat Ala Glu His	tta tcg gat Leu Ser Asp 30	96
atc gga atc Ile Gly Ile 35	act gcc	gtc tgg att Val Trp Ile 40	e Pro Pro	gca tac aaa Ala Tyr Lys 45	gga ttg agc Gly Leu Ser	144
caa tcc gat Gln Ser Asp 50	aac gga n Asn Gly	tac gga cct Tyr Gly Pro 55	tat gat Tyr Asp	ttg tat gat Leu Tyr Asp 60	tta gga gaa Leu Gly Glu	192
ttc cag caa Phe Gln Gln 65	aaa ggg a Lys Gly 3	acg gtc aga Thr Val Arc 70	a acg aaa Thr Lys	tac ggc aca Tyr Gly Thr 75	aaa gga gag Lys Gly Glu 80	240
ctg caa tct Leu Gln Ser	gcg atc a Ala Ile I 85	aaa agt ctt Lys Ser Leu	cat tcc His Ser 90	cgc gac att Arg Asp Ile	aac gtt tac Asn Val Tyr 95	288
ggg gat gtg Gly Asp Val	gtc atc a Val Ile A 100	aac cac aaa Asn His Lys	ggc ggc Gly Gly 105	gct gat gcg Ala Asp Ala	acc gaa gat Thr Glu Asp 110	336
gta acc gcg Val Thr Ala 115	gtt gaa g Val Glu V	tc gat ccc al Asp Pro 120	Ala Asp	cgc aac cgc Arg Asn Arg 125	gta att tca Val Ile Ser	384
gga gaa cac Gly Glu His 130	cga att a Arg Ile L	aa gcc tgg ys Ala Trp 135	aca cat Thr His	ttt cat ttt Phe His Phe 140	ccg ggg cgc Pro Gly Arg	432
ggc agc aca Gly Ser Thr 145	Tyr Ser A	at ttt aaa sp Phe Lys 50	Trp His	tgg tac cat Trp Tyr His 155	ttt gac gga Phe Asp Gly 160	480
acc gat tgg ( Thr Asp Trp )	gac gag t Asp Glu S 165	cc cga aag er Arg Lys	ctg aac Leu Asn 1	cgc atc tat Arg Ile Tyr	aag ttt caa Lys Phe Gln 175	528
gga aag gct f Gly Lys Ala :	tgg gat to Trp Asp T 180	gg gaa gtt rp Glu Val	tcc aat of Ser Asn of 185	gaa aac ggc Glu Asn Gly	aac tat gat Asn Tyr Asp 190	576
tat ttg atg t Tyr Leu Met 1 195	tat gcc ga Tyr Ala As	ac atc gat sp Ile Asp 200	tat gac o Tyr Asp 1	cat cct gat His Pro Asp 205	gtc gca gca Val Ala Ala	624
gaa att aag a Glu Ile Lys A 210	aga tgg gg Arg Trp G	gc act tgg Ly Thr Trp 215	tat gcc a Tyr Ala A	aat gaa ctg Asn Glu Leu 220	caa ttg gac ( Gln Leu Asp	672

ggt Gly 225	Phe	c cgt	t ctt g Lei	gat 1 Asi	t gct P Ala 230	. Val	aaa L Lys	a cad s His	att Ile	aaa Lys 235	Phe	tct Ser	ttt Phe	ttq Le	g cgg 1 Arg 240	720
gat Asp	tgg Trp	ggtt Val	aat L Asr	cat His 245	yal (	agg Arg	g gaa g Glu	aaa Lys	aco Thr 250	: Gly	aaq Lys	g gaa Glu	ato Met	ttt Phe 255	acg Thr	768
gta Val	gct Ala	gaa Glu	tat Tyr 260	Trp	g cag Gln	aat Asn	gac Asp	ttg Leu 265	Gly	geg Ala	ctg Leu	gaa Glu	aac Asn 270	Tyr	ttg Leu	816
aac Asn	aaa Lys	aca Thr 275	Asn	ttt Phe	aat Asn	cat His	tca Ser 280	Val	ttt Phe	gac Asp	gtg Val	ccg Pro 285	ctt Leu	cat His	tat Tyr	864
cag Gln	ttc Phe 290	His	gct Ala	gca Ala	tcg Ser	aca Thr 295	cag Gln	gga Gly	ggc Gly	ggc	tat Tyr 300	Asp	atg Met	agg Arg	aaa Lys	912
ttg Leu 305	ctg Leu	aac Asn	agt Ser	acg Thr	gtc Val 310	gtt Val	tcc Ser	aag Lys	cat His	ccg Pro 315	ttg Leu	aaa Lys	gcg Ala	gtt Val	aca Thr 320	960
ttt Phe	gtc Val	gat Asp	aac Asn	cat His 325	gat Asp	aca Thr	cag Gln	ccg Pro	ggg Gly 330	caa Gln	tcg Ser	ctt Leu	gag Glu	tcg Ser 335	act Thr	1008
gtc Val	caa Gln	aca Thr	tgg Trp 340	ttt Phe	aag Lys	ccg Pro	ctt Leu	gct Ala 345	tac Tyr	gct Ala	ttt Phe	att Ile	ctc Leu 350	aca Thr	agg Arg	1056
gaa Glu	tct Ser	gga Gly 355	tac Tyr	cct Pro	cag Gln	gtt Val	ttc Phe 360	tac Tyr	ggg Gly	gat Asp	atg Met	tac Tyr 365	ggg Gly	acg Thr	aaa Lys	1104
gga Gly	gac Asp 370	tcc Ser	cag Gln	cgc Arg	gaa Glu	att Ile 375	cct Pro	gcc Ala	ttg Leu	aaa Lys	cac His 380	aaa Lys	att Ile	gaa Glu	ccg Pro	1152
atc Ile 385	tta Leu	a <b>a</b> a Lys	gcg Ala	aga Arg	aaa Lys 390	cag Gln	tat Tyr	gcg Ala	tac Tyr	gga Gly 395	gca Ala	cag Gln	cat His	gat Asp	tat Tyr 400	1200
ttc Phe	gac Asp	cac His	cat His	gac Asp 405	att Ile	gtc Val	ggc Gly	tgg Trp	aca Thr 410	agg Arg	gaa Glu	ggc Gly	gac Asp	agc Ser 415	tcg Ser	1248
gtt Val	gca Ala	aat Asn	tca Ser 420	ggt Gly	ttg Leu	gcg Ala	gca Ala	tta Leu 425	ata Ile	aca Thr	gac Asp	gga Gly	ccc Pro 430	ggt Gly	G] À āāā	1296
gca Ala	гàг	cga Arg 435	atg Met	tat Tyr	gtc Val	ggc Gly	cgg Arg 440	caa Gln	aac Asn	gcc Ala	ggt Gly	gag Glu 445	aca Thr	tgg Trp	cat His	1344
gac Asp	att Ile	acc Thr	gga Gly	aac Asn	cgt Arg	tcg Ser	gag Glu	ccg Pro	gtt Val	gtc Val	atc Ile	aat Asn	tcg Ser	gaa Glu	ggc	1392

310

450 455 460 tgg gga gag ttt cac gta aac ggc ggg tcg gtt tca att tat gtt caa 1440 Trp Gly Glu Phe His Val Asn Gly Gly Ser Val Ser Ile Tyr Val Gln 470 475 aga tag 1446 Arg <210> 8 <211> 481 <212> PRT <213> Künstliche Sequenz <223> Beschreibung der künstlichen Sequenz: Fusion der Alpha-Amylase-Gene von B. licheniformis und B. amyloliquefaciens (AL76). <400> 8 Val Asn Gly Thr Leu Met Gln Tyr Phe Glu Trp Tyr Thr Pro Asn Asp Gly Gln His Trp Lys Arg Leu Gln Asn Asp Ala Glu His Leu Ser Asp 20 Ile Gly Ile Thr Ala Val Trp Ile Pro Pro Ala Tyr Lys Gly Leu Ser Gln Ser Asp Asn Gly Tyr Gly Pro Tyr Asp Leu Tyr Asp Leu Gly Glu 55 60 Phe Gln Gln Lys Gly Thr Val Arg Thr Lys Tyr Gly Thr Lys Gly Glu Leu Gln Ser Ala Ile Lys Ser Leu His Ser Arg Asp Ile Asn Val Tyr 90 Gly Asp Val Val Ile Asn His Lys Gly Gly Ala Asp Ala Thr Glu Asp 105 Val Thr Ala Val Glu Val Asp Pro Ala Asp Arg Asn Arg Val Ile Ser 115 120 125 Gly Glu His Arg Ile Lys Ala Trp Thr His Phe His Phe Pro Gly Arg 135 140 Gly Ser Thr Tyr Ser Asp Phe Lys Trp His Trp Tyr His Phe Asp Gly 150 155 Thr Asp Trp Asp Glu Ser Arg Lys Leu Asn Arg Ile Tyr Lys Phe Gln 165 170 Gly Lys Ala Trp Asp Trp Glu Val Ser Asn Glu Asn Gly Asn Tyr Asp 180 185 Tyr Leu Met Tyr Ala Asp Ile Asp Tyr Asp His Pro Asp Val Ala Ala 200 Glu Ile Lys Arg Trp Gly Thr Trp Tyr Ala Asn Glu Leu Gln Leu Asp 215 220 Gly Phe Arg Leu Asp Ala Val Lys His Ile Lys Phe Ser Phe Leu Arg 230 235 Asp Trp Val Asn His Val Arg Glu Lys Thr Gly Lys Glu Met Phe Thr 245 250 Val Ala Glu Tyr Trp Gln Asn Asp Leu Gly Ala Leu Glu Asn Tyr Leu 260 265 270 Asn Lys Thr Asn Phe Asn His Ser Val Phe Asp Val Pro Leu His Tyr 275 280 285 Gln Phe His Ala Ala Ser Thr Gln Gly Gly Gly Tyr Asp Met Arg Lys 295 300 Leu Leu Asn Ser Thr Val Val Ser Lys His Pro Leu Lys Ala Val Thr

Phe Val Asp Asn His Asp Thr Gln Pro Gly Gln Ser Leu Glu Ser Thr 325 330 Val Gln Thr Trp Phe Lys Pro Leu Ala Tyr Ala Phe Ile Leu Thr Arg 345 350 Glu Ser Gly Tyr Pro Gln Val Phe Tyr Gly Asp Met Tyr Gly Thr Lys 360 365. Gly Asp Ser Gln Arg Glu Ile Pro Ala Leu Lys His Lys Ile Glu Pro 375 380 Ile Leu Lys Ala Arg Lys Gln Tyr Ala Tyr Gly Ala Gln His Asp Tyr 390 395 Phe Asp His His Asp Ile Val Gly Trp Thr Arg Glu Gly Asp Ser Ser 405 410 Val Ala Asn Ser Gly Leu Ala Ala Leu Ile Thr Asp Gly Pro Gly Gly 420 425 Ala Lys Arg Met Tyr Val Gly Arg Gln Asn Ala Gly Glu Thr Trp His 435 440 445 Asp Ile Thr Gly Asn Arg Ser Glu Pro Val Val Ile Asn Ser Glu Gly 455 460 Trp Gly Glu Phe His Val Asn Gly Gly Ser Val Ser Ile Tyr Val Gln 470 475 Arg <210> 9 <211> 1446 <212> DNA <213> Künstliche Sequenz <220> <223> Beschreibung der künstlichen Sequenz:Fusion der Alpha-Amylase-Gene von B. licheniformis und B. amyloliquefaciens (AL112). <220> <221> CDS <222> (1)..(1446)

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ggc cag cat tgg aaa cga ttg cag aat gat gcg gaa cat tta tcg gat Gly Gln His Trp Lys Arg Leu Gln Asn Asp Ala Glu His Leu Ser Asp 25

atc gga atc act gcc gtc tgg att cct ccc gca tac aaa gga ttg agc 144 Ile Gly Ile Thr Ala Val Trp Ile Pro Pro Ala Tyr Lys Gly Leu Ser 40

caa too gat aac gga tac gga cot tat gat ttg tat gat tta gga gaa 192 Gin Ser Asp Asn Gly Tyr Gly Pro Tyr Asp Leu Tyr Asp Leu Gly Glu 55

ttc cag caa aaa ggg acg gtc aga acg aaa tac ggc aca aaa tca gag 240 Phe Gln Gln Lys Gly Thr Val Arg Thr Lys Tyr Gly Thr Lys Ser Glu 75

ctt Leu	caa Gln	gat Asp	gcg Ala	ato Ile 85	Gly	tca Ser	ctg Leu	cat His	tcc Ser 90	Arg	aac Asn	gto Val	caa Gln	gta Val	tac Tyr	288
gga Gly	gat Asp	gtg Val	gtt Val 100	Leu	aat Asn	cat His	aag Lys	gct Ala 105	Gly	gct Ala	gat Asp	gca Ala	aca Thr 110	Glu	gat Asp	336
gta Val	acc Thr	gcg Ala 115	gtt Val	gaa Glu	gtc Val	gat Asp	ccc Pro 120	Ala	gac Asp	cgc Arg	aac	cgc Arg 125	Val	att	tca Ser	384
gga Gly	gaa Glu 130	cac His	cga Arg	att Ile	aaa Lys	gcc Ala 135	tgg Trp	aca Thr	cat His	ttt Phe	cat His 140	Phe	ccg Pro	ggg	cgc Arg	432
ggc Gly 145	agc Ser	aca Thr	tac Tyr	agc Ser	gat Asp 150	ttt Phe	aaa Lys	tgg Trp	cat His	tgg Trp 155	tac Tyr	cat His	ttt Phe	gac Asp	gga Gly 160	480
acc Thr	gat Asp	tgg Trp	gac Asp	gag Glu 165	tcc Ser	cga Arg	aag Lys	ctg Leu	aac Asn 170	cgc Arg	atc Ile	tat Tyr	aag Lys	ttt Phe 175	caa Gln	528
gga Gly	aag Lys	gct Ala	tgg Trp 180	gat Asp	tgg Trp	gaa Glu	gtt Val	tcc Ser 185	aat Asn	gaa Glu	aac Asn	Gly	aac Asn 190	tat Tyr	gat Asp	576
tat Tyr	ttg Leu	atg Met 195	tat Tyr	gcc Ala	gac Asp	atc Ile	gat Asp 200	tat Tyr	gac Asp	cat His	cct Pro	gat Asp 205	gtc Val	gca Ala	gca Ala	624
gaa Glu	att Ile 210	aag Lys	aga Arg	tgg Trp	ggc Gly	act Thr 215	tgg Trp	tat Tyr	gcc Ala	aat Asn	gaa Glu 220	ctg Leu	caa Gln	ttg Leu	gac Asp	672
ggt Gly 225	ttc Phe	cgt Arg	ctt Leu	gat Asp	gct Ala 230	gtc Val	aaa Lys	cac His	att Ile	aaa Lys 235	ttt Phe	tct Ser	ttt Phe	ttg Leu	cgg Arg 240	720
gat Asp	tgg Trp	gtt Val	aat Asn	cat His 245	gtc Val	agg Arg	gaa Glu	aaa Lys	acg Thr 250	ggg Gly	aag Lys	gaa Glu	atg Met	ttt Phe 255	acg Thr	768
gta Val	gct Ala	gaa Glu	tat Tyr 260	tgg Trp	cag Gln	aat Asn	gac Asp	ttg Leu 265	ggc Gly	gcg Ala	ctg Leu	gaa Glu	aac Asn 270	tat Tyr	ttg Leu	816
aac Asn	aaa Lys	aca Thr 275	aat Asn	ttt Phe	aat Asn	cat His	tca Ser 280	gtg Val	ttt Phe	gac Asp	gtg Val	ccg Pro 285	ctt Leu	cat His	tat Tyr	864
cag Gln	ttc Phe 290	cat His	gct Ala	gca Ala	tcg Ser	aca Thr 295	cag Gln	gga Gly	ggc Gly	ggc Gly	tat Tyr 300	gat Asp	atg Met	agg Arg	aaa Lys	912
ttg Leu 305	ctg Leu	aac Asn	agt Ser	acg Thr	gtc Val 310	gtt Val	tcc Ser	aag Lys	cat His	ccg Pro 315	ttg Leu	aaa Lys	gcg Ala	gtt Val	aca Thr 320	960

ttt Phe	gtc Val	gat Asp	aac Asn	cat His 325	gat Asp	aca Thr	cag Gln	ccg Pro	ggg 330	caa Gln	tcg Ser	ctt Leu	gag Glu	tcg Ser 335	Thr	1008
gtc Val	caa Gln	aca Thr	tgg Trp 340	ttt Phe	aag Lys	ccg Pro	ctt Leu	gct Ala 345	Tyr	gct Ala	ttt Phe	att Ile	ctc Leu 350	aca Thr	agg Arg	1056
gaa Glu	tct Ser	gga Gly 355	tac Tyr	cct Pro	cag Gln	gtt Val	ttc Phe 360	tac Tyr	ggg	gat Asp	atg Met	tac Tyr 365	G]A aaa	acg Thr	aaa Lys	1104
gga Gly	gac Asp 370	tcc Ser	cag Gln	cgc Arg	gaa Glu	att Ile 375	cct Pro	gcc Ala	ttg Leu	aaa Lys	cac His 380	aaa Lys	att Ile	gaa Glu	ccg Pro	1152
atc Ile 385	tta Leu	aaa Lys	gcg Ala	aga Arg	aaa Lys 390	cag Gln	tat Tyr	gcg Ala	tac Tyr	gga Gly 395	gca Ala	cag Gln	cat His	gat Asp	tat Tyr 400	1200
ttc Phe	gac Asp	cac His	cat His	gac Asp 405	att Ile	gtc Val	ggc Gly	tgg Trp	aca Thr 410	agg Arg	gaa Glu	ggc Gly	gac Asp	agc Ser 415	tcg Ser	1248
gtt Val	gca Ala	aat Asn	tca Ser 420	ggt Gly	ttg Leu	gcg Ala	gca Ala	tta Leu 425	ata Ile	aca Thr	gac Asp	gga Gly	ccc Pro 430	ggt Gly	Gly ggg	1296
gca Ala	aag Lys	cga Arg 435	atg Met	tat Tyr	gtc Val	ggc Gly	cgg Arg 440	caa Gln	aac Asn	gcc Ala	ggt Gly	gag Glu 445	aca Thr	tgg Trp	cat His	1344
gac Asp	att Ile 450	acc Thr	gga Gly	aac Asn	cgt Arg	tcg Ser 455	gag Glu	ccg Pro	gtt Val	gtc Val	atc Ile 460	aat Asn	tcg Ser	gaa Glu	ggc Gly	1392
tgg Trp 465	gga Gly	gag Glu	ttt Phe	cac His	gta Val 470	aac Asn	ggc Gly	ggg Gly	tcg Ser	gtt Val 475	tca Ser	att Ile	tat Tyr	gtt Val	caa Gln 480	1440
aga Arg	tag															1446

<210> 10

<211> 481

<212> PRT

<213> Künstliche Sequenz

<223> Beschreibung der künstlichen Sequenz:Fusion der Alpha-Amylase-Gene von B. licheniformis und B. amyloliquefaciens (AL112).

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Val Asn Gly Thr Leu Met Gln Tyr Phe Glu Trp Tyr Thr Pro Asn Asp 1 . 5 . 5 . 10 . 15 . 15 . Gly Gln His Trp Lys Arg Leu Gln Asn Asp Ala Glu His Leu Ser Asp 20 . 25 . 25 . 25 . 30 . Ile Gly Ile Thr Ala Val Trp Ile Pro Pro Ala Tyr Lys Gly Leu Ser

40 Gln Ser Asp Asn Gly Tyr Gly Pro Tyr Asp Leu Tyr Asp Leu Gly Glu 55 Phe Gln Gln Lys Gly Thr Val Arg Thr Lys Tyr Gly Thr Lys Ser Glu Leu Gln Asp Ala Ile Gly Ser Leu His Ser Arg Asn Val Gln Val Tyr Gly Asp Val Val Leu Asn His Lys Ala Gly Ala Asp Ala Thr Glu Asp 105 Val Thr Ala Val Glu Val Asp Pro Ala Asp Arg Asn Arg Val Ile Ser 120 Gly Glu His Arg Ile Lys Ala Trp Thr His Phe His Phe Pro Gly Arg 135 Gly Ser Thr Tyr Ser Asp Phe Lys Trp His Trp Tyr His Phe Asp Gly 150 155 Thr Asp Trp Asp Glu Ser Arg Lys Leu Asn Arg Ile Tyr Lys Phe Gln 165 170 Gly Lys Ala Trp Asp Trp Glu Val Ser Asn Glu Asn Gly Asn Tyr Asp 185 Tyr Leu Met Tyr Ala Asp Ile Asp Tyr Asp His Pro Asp Val Ala Ala 200 Glu Ile Lys Arg Trp Gly Thr Trp Tyr Ala Asn Glu Leu Gln Leu Asp 215 220 Gly Phe Arg Leu Asp Ala Val Lys His Ile Lys Phe Ser Phe Leu Arg 230 235 Asp Trp Val Asn His Val Arg Glu Lys Thr Gly Lys Glu Met Phe Thr 245 250 Val Ala Glu Tyr Trp Gln Asn Asp Leu Gly Ala Leu Glu Asn Tyr Leu 265 Asn Lys Thr Asn Phe Asn His Ser Val Phe Asp Val Pro Leu His Tyr 280 285 Gln Phe His Ala Ala Ser Thr Gln Gly Gly Gly Tyr Asp Met Arg Lys 295 300 Leu Leu Asn Ser Thr Val Val Ser Lys His Pro Leu Lys Ala Val Thr 310 315 Phe Val Asp Asn His Asp Thr Gln Pro Gly Gln Ser Leu Glu Ser Thr 325 330 Val Gln Thr Trp Phe Lys Pro Leu Ala Tyr Ala Phe Ile Leu Thr Arg 345 Glu Ser Gly Tyr Pro Gln Val Phe Tyr Gly Asp Met Tyr Gly Thr Lys 360 Gly Asp Ser Gln Arg Glu Ile Pro Ala Leu Lys His Lys Ile Glu Pro 375 380 Ile Leu Lys Ala Arg Lys Gln Tyr Ala Tyr Gly Ala Gln His Asp Tyr 390 395 Phe Asp His His Asp Ile Val Gly Trp Thr Arg Glu Gly Asp Ser Ser 410 Val Ala Asn Ser Gly Leu Ala Ala Leu Ile Thr Asp Gly Pro Gly Gly 420 425 Ala Lys Arg Met Tyr Val Gly Arg Gln Asn Ala Gly Glu Thr Trp His 440 Asp Ile Thr Gly Asn Arg Ser Glu Pro Val Val Ile Asn Ser Glu Gly 455 460 Trp Gly Glu Phe His Val Asn Gly Gly Ser Val Ser Ile Tyr Val Gln 465 470 475 Arg

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<210> 11
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<212> DNA
<213> Künstliche Sequenz
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<223> Beschreibung der künstlichen Sequenz: Fusion der
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      amyloliquefaciens (AL256).
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ggc cag cat tgg aaa cga ttg cag aat gat gcg gaa cat tta tcg gat
                                                                    96
Gly Gln His Trp Lys Arg Leu Gln Asn Asp Ala Glu His Leu Ser Asp
             20
atc gga atc act gcc gtc tgg att cct ccc gca tac aaa gga ttg agc
                                                                    144
Ile Gly Ile Thr Ala Val Trp Ile Pro Pro Ala Tyr Lys Gly Leu Ser
caa tcc gat aac gga tac gga cct tat gat ttg tat gat tta gga gaa
                                                                    192
Gln Ser Asp Asn Gly Tyr Gly Pro Tyr Asp Leu Tyr Asp Leu Gly Glu
ttc cag caa aaa ggg acg gtc aga acg aaa tac ggc aca aaa tca gag
                                                                    240
Phe Gln Gln Lys Gly Thr Val Arg Thr Lys Tyr Gly Thr Lys Ser Glu
                     70
ctt caa gat gcg atc ggc tca ctg cat tcc cgg aac gtc caa gta tac
                                                                    288
Leu Gln Asp Ala Ile Gly Ser Leu His Ser Arg Asn Val Gln Val Tyr
                 85
gga gat gtg gtt ttg aat cat aag gct ggt gct gat gca aca gaa gat
                                                                   336
Gly Asp Val Val Leu Asn His Lys Ala Gly Ala Asp Ala Thr Glu Asp
            100
gta act gcc gtc gaa gtc aat ccg gcc aat aga aat cag gaa act tcg
                                                                   384
Val Thr Ala Val Glu Val Asn Pro Ala Asn Arg Asn Gln Glu Thr Ser
                            120
gag gaa tat caa atc aaa gcg tgg acg gat ttt cgt ttt ccg ggc cgt
                                                                   432
Glu Glu Tyr Gln Ile Lys Ala Trp Thr Asp Phe Arg Phe Pro Gly Arg
                        135
gga aac acg tac agt gat ttt aaa tgg cat tgg tat cat ttc gac gga
                                                                   480
Gly Asn Thr Tyr Ser Asp Phe Lys Trp His Trp Tyr His Phe Asp Gly
                    150
                                        155
gcg gac tgg gat gaa tcc cgg aag atc agc cgc atc ttt aag ttt cgt
                                                                   528
Ala Asp Trp Asp Glu Ser Arg Lys Ile Ser Arg Ile Phe Lys Phe Arg
                165
                                    170
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				Ala					Val					Ğİy	aac Asn	576
tat Tyr	gac Asp	tat Tyr 195	Leu	atg Met	tat Tyr	gct Ala	gat Asp 200	Val	gac Asp	tac Tyr	gac	Cac His 205	Pro	gat Asp	gtc Val	624
gtg Val	gca Ala 210	Glu	aca Thr	aaa Lys	aaa Lys	tgg Trp 215	Gly	atc Ile	tgg Trp	tat Tyr	gcg Ala 220	Asn	gaa Glu	ctg Leu	tca Ser	672
tta Leu 225	gac Asp	ggc	ttc Phe	cgt Arg	att Ile 230	gat Asp	gcc Ala	gcc Ala	aaa Lys	cat His 235	att Ile	aaa Lys	ttt Phe	tca Ser	ttt Phe 240	720
ctg Leu	cgt Arg	gat Asp	tgg Trp	gtt Val 245	cag Gln	gcg Ala	gtc Val	aga Arg	cag Gln 250	gcg Ala	acg Thr	gga Gly	aaa Lys	gaa Glu 255	atg Met	768
ttt Phe	acg Thr	gta Val	gct Ala 260	gaa Glu	tat Tyr	tgg Trp	cag Gln	aat Asn 265	gac Asp	ttg Leu	Gly	gcg Ala	ctg Leu 270	gaa Glu	aac Asn	816
tat Tyr	ttg Leu	aac Asn 275	aaa Lys	aca Thr	aat Asn	ttt Phe	aat Asn 280	cat His	tca Ser	gtg Val	ttt Phe	gac Asp 285	gtg Val	ccg Pro	ctt Leu	864
cat His	tat Tyr 290	cag Gln	ttc Phe	cat His	gct Ala	gca Ala 295	tcg Ser	aca Thr	cag Gln	gga Gly	ggc Gly 300	ggc Gly	tat Tyr	gat Asp	atg Met	912
agg Arg 305	aaa Lys	ttg Leu	ctg Leu	aac Asn	agt Ser 310	acg Thr	gtc Val	gtt Val	tcc Ser	aag Lys 315	cat His	ccg Pro	ttg Leu	aaa Lys	gcg Ala 320	960
gtt Val	aca Thr	ttt Phe	gtc Val	gat Asp 325	aac Asn	cat His	gat Asp	aca Thr	cag Gln 330	ccg Pro	Gly	caa Gln	tcg Ser	ctt Leu 335	gag Glu	1008
tcg Ser	act Thr	gtc Val	caa Gln 340	aca Thr	tgg Trp	ttt Phe	aag Lys	ccg Pro 345	ctt Leu	gct Ala	tac Tyr	gct Ala	ttt Phe 350	att Ile	ctc Leu	1056
aca Thr	agg Arg	gaa Glu 355	tct Ser	gga Gly	tac Tyr	cct Pro	cag Gln 360	gtt Val	ttc Phe	tac Tyr	Gly ggg	gat Asp 365	atg Met	tac Tyr	G] À Gàà	1104
acg Thr	aaa Lys 370	gga Gly	gac Asp	tcc Ser	cag Gln	cgc Arg 375	gaa Glu	att Ile	cct Pro	gcc Ala	ttg Leu 380	aaa Lys	cac His	aaa Lys	att Ile	1152
gaa Glu 385	ccg Pro	atc Ile	tta Leu	aaa Lys	gcg Ala 390	aga Arg	aaa Lys	cag Gln	tat Tyr	gcg Ala 395	tac Tyr	gga Gly	gca Ala	Gln	cat His 400	1200
gat Asp	tat Tyr	ttc Phe	gac Asp	cac His 405	cat His	gac Asp	att Ile	Val	ggc Gly 410	tgg Trp	aca Thr	agg Arg	gaa Glu	ggc Gly 415	gac Asp	1248

			gca Ala 420													1296
			aag Lys													1344
tgg Trp	cat His 450	gac Asp	att Ile	acc Thr	gga Gly	aac Asn 455	cgt Arg	tcg Ser	gag Glu	ccg Pro	gtt Val 460	gtc Val	atc Ile	aat Asn	tcg Ser	1392
gaa Glu 465	ggc Gly	tgg Trp	gga Gly	gag Glu	ttt Phe 470	cac His	gta Val	aac Asn	ggc Gly	ggg Gly 475	tcg Ser	gtt Val	tca Ser	att Ile	tat Tyr 480	1440
	caa Gln	aga Arg	tag					•								1452

<21Ó> 12

<211> 483

<212> PRT

<213> Künstliche Sequenz

<223> Beschreibung der künstlichen Sequenz: Fusion der Alpha-Amylase-Gene von B. licheniformis und B. amyloliquefaciens (AL256).

<400> 12 Val Asn Gly Thr Leu Met Gln Tyr Phe Glu Trp Tyr Thr Pro Asn Asp 10 Gly Gln His Trp Lys Arg Leu Gln Asn Asp Ala Glu His Leu Ser Asp 25 Ile Gly Ile Thr Ala Val Trp Ile Pro Pro Ala Tyr Lys Gly Leu Ser 40 Gln Ser Asp Asn Gly Tyr Gly Pro Tyr Asp Leu Tyr Asp Leu Gly Glu 55 Phe Gln Gln Lys Gly Thr Val Arg Thr Lys Tyr Gly Thr Lys Ser Glu 70 Leu Gln Asp Ala Ile Gly Ser Leu His Ser Arg Asn Val Gln Val Tyr 85 Gly Asp Val Val Leu Asn His Lys Ala Gly Ala Asp Ala Thr Glu Asp 100 105 110 Val Thr Ala Val Glu Val Asn Pro Ala Asn Arg Asn Gln Glu Thr Ser 120 125 Glu Glu Tyr Gln Ile Lys Ala Trp Thr Asp Phe Arg Phe Pro Gly Arg 135 140 Gly Asn Thr Tyr Ser Asp Phe Lys Trp His Trp Tyr His Phe Asp Gly 150 155 Ala Asp Trp Asp Glu Ser Arg Lys Ile Ser Arg Ile Phe Lys Phe Arg 165 170 Gly Glu Gly Lys Ala Trp Asp Trp Glu Val Ser Ser Glu Asn Gly Asn 180 185 Tyr Asp Tyr Leu Met Tyr Ala Asp Val Asp Tyr Asp His Pro Asp Val 195 200 Val Ala Glu Thr Lys Lys Trp Gly Ile Trp Tyr Ala Asn Glu Leu Ser 215

Leu Asp Gly Phe Arg Ile Asp Ala Ala Lys His Ile Lys Phe Ser Phe

<210> 13

Leu Arg Asp Trp Val Gln Ala Val Arg Gln Ala Thr Gly Lys Glu Met Phe Thr Val Ala Glu Tyr Trp Gln Asn Asp Leu Gly Ala Leu Glu Asn Tyr Leu Asn Lys Thr Asn Phe Asn His Ser Val Phe Asp Val Pro Leu His Tyr Gln Phe His Ala Ala Ser Thr Gln Gly Gly Gly Tyr Asp Met Arg Lys Leu Leu Asn Ser Thr Val Val Ser Lys His Pro Leu Lys Ala Val Thr Phe Val Asp Asn His Asp Thr Gln Pro Gly Gln Ser Leu Glu Ser Thr Val Gln Thr Trp Phe Lys Pro Leu Ala Tyr Ala Phe Ile Leu Thr Arg Glu Ser Gly Tyr Pro Gln Val Phe Tyr Gly Asp Met Tyr Gly Thr Lys Gly Asp Ser Gln Arg Glu Ile Pro Ala Leu Lys His Lys Ile Glu Pro Ile Leu Lys Ala Arg Lys Gln Tyr Ala Tyr Gly Ala Gln His Asp Tyr Phe Asp His His Asp Ile Val Gly Trp Thr Arg Glu Gly Asp Ser Ser Val Ala Asn Ser Gly Leu Ala Ala Leu Ile Thr Asp Gly Pro Gly Gly Ala Lys Arg Met Tyr Val Gly Arg Gln Asn Ala Gly Glu Thr Trp His Asp Ile Thr Gly Asn Arg Ser Glu Pro Val Val Ile Asn Ser Glu Gly Trp Gly Glu Phe His Val Asn Gly Gly Ser Val Ser Ile Tyr Val Gln Arg

Gly Gln His Trp Lys Arg Leu Gln Asn Asp Ala Glu His Leu Ser Asp

atc ggt att act gcc gtc tgg att ccc ccg gca tat aag gga acg agc

.Il	e -Gl	y Il.	e Thi	r Ala	a Va	l Tr	2 Ile 40		Pr	o Ala	а Ту	r Ly:		y Th	r Ser	
caa Gl:	a gco n Ala 50	a Ası	t gto p Val	g ggo	c tac y Ty	ggt Gly 5	/ Ala	tad Tyr	gad Ası	c ctt	t tai 1 Ty:	r Asp	t tta	a gg u Gl	g gag y Glu	192
ttt Phe 65	HIS	caa Gli	a aaa n Lys	g Gl	g aco Thi	. Val	cgc Arc	g aca g Thr	aaq Lys	tac Tyr 75	Gly	c aca y Thi	a aaa Lys	a gg	a gag y Glu 80	240
cto Lev	g caa g Glr	tct Ser	gco Ala	ato Ile 85	s CT?	tca Ser	Leu	cat His	Ser 90	Arg	aac Asr	gto Val	caa Glr	a gta 1 Va: 9	a tac l Tyr	288
gga Gly	gat Asp	gto Val	g gtt Val 100	ьeu	aat Asn	cat His	aag Lys	gct Ala 105	ggt Gly	gct Ala	gat Asp	gca Ala	aca Thr 110	Glu	a gat 1 Asp	336
gta Val	act Thr	gcc Ala 115	vaı	gaa Glu	gtc Val	aat Asn	ccg Pro 120	gcc Ala	aat Asn	aga Arg	aat Asn	cag Gln 125	Glu	act Thr	tcg Ser	384
gag Glu	gaa Glu 130	Tyr	caa Gln	atc Ile	aaa Lys	gcg Ala 135	tgg Trp	acg Thr	gat Asp	ttt Phe	cgt Arg 140	Phe	ccg Pro	Gl}	cgt Arg	432
145	Asn	Thr	Tyr	Ser	Asp 150	Phe	Lys	Trp	His	Trp 155	Tyr	His	Phe	Asp	gga Gly 160	480
gcg Ala	gac Asp	tgg Trp	gat Asp	gaa Glu 165	tcc Ser	cgg Arg	aag Lys	atc Ile	agc Ser 170	cgc Arg	atc Ile	ttt Phe	aag Lys	ttt Phe 175	cgt Arg	528
G] À aaa	gaa Glu	gga Gly	aaa Lys 180	gcg Ala	tgg Trp	gat Asp	tgg Trp	gaa Glu 185	gta Val	tca Ser	agt Ser	gaa Glu	aac Asn 190	ggc	aac Asn	576
tat Tyr	Asp	tat Tyr 195	tta Leu	Met	tat Tyr	Ala	Asp	Val	gac Asp	tac Tyr	gac Asp	cac His 205	cct Pro	gat Asp	gtc Val	624
gtg Val	gca Ala 210	gag Glu	aca Thr	aaa Lys	aaa Lys	tgg Trp 215	ggt Gly	atc Ile	tgg Trp	tat Tyr	gcg Ala 220	aat Asn	gaa Glu	ctg Leu	tca Ser	672
tta Leu 225	gac Asp	ggc	ttc Phe	cgt Arg	att Ile 230	gat Asp	gcc Ala	gcc Ala	aaa Lys	cat His 235	att Ile	aaa Lys	ttt Phe	tca Ser	ttt Phe 240	720
ctg Leu	cgt Arg	gat Asp	tgg Trp	gtt Val 245	cag Gln	gcg Ala	gtc Val	Arg	cag Gln 250	gcg Ala	acg Thr	gga Gly	aaa Lys	gaa Glu 255	atg Met	768
ttt Phe	acg Thr	gtt Val	gcg Ala 260	gag Glu	tat Tyr	tgg Trp	Gin .	aat Asn . 265	aat Asn	gcc Ala	ggg Gly	Lys	ctc Leu 270	gaa Glu	aac Asn	816

tac Tyr	ttg Leu	aat Asn 275	Lys	aca Thr	agc Ser	ttt Phe	aat Asn 280	Gln	tcc Ser	gtg Val	ttt Phe	gat Asp 285	Val	ccg Pro	ctt Leu	864
cat His	ttc Phe 290	Asn	tta Leu	cag Gln	gcg Ala	gct Ala 295	tcc Ser	tca Ser	caa Gln	gga Gly	Gly 300	Gly	tat Tyr	gat Asp	atg Met	912
agg Arg 305	Arg	ttg Leu	ctg Leu	gac Asp	ggt Gly 310	acc Thr	gtt Val	gtg Val	tcc Ser	agg Arg 315	cat His	ccg Pro	gaa Glu	aag Lys	gcg Ala 320	960
gtt Val	aca Thr	ttt Phe	gtt Val	gaa Glu 325	aat Asn	cat His	gac Asp	aca Thr	cag Gln 330	ccg Pro	gga Gly	cag Gln	tca Ser	ttg Leu 335	gaa Glu	1008
tcg Ser	aca Thr	gtc Val	caa Gln 340	act Thr	tgg Trp	ttt Phe	aaa Lys	ccg Pro 345	ctt Leu	gca Ala	tac Tyr	gcc Ala	ttt Phe 350	att Ile	ttg Leu	1056
aca Thr	aga Arg	gaa Glu 355	tcc Ser	ggt Gly	tat T <u>y</u> r	cct Pro	cag Gln 360	gtg Val	ttc Phe	tat Tyr	Gly	gat Asp 365	atg Met	tac Tyr	Gly ggg	1104
Thr	Lys 370	Gly	Thr	Ser	cca Pro	Lys 375	Glu	Ile	Pro	Ser	Leu 380	Lys	Asp	Asn	Ile	1152
gag Glu 385	ccg Pro	att Ile	tta Leu	aaa Lys	gcg Ala 390	cgt Arg	aag Lys	gag Glu	tac Tyr	gca Ala 395	tac Tyr	Gly ggg	ccc Pro	cag Gln	cac His 400	1200
gat Asp	tat Tyr	att Ile	gac Asp	cac His 405	ccg Pro	gat Asp	gtg Val	atc Ile	gga Gly 410	tgg Trp	acg Thr	agg Arg	gaa Glu	ggt Gly 415	gac Asp	1248
agc Ser	tcc Ser	gcc Ala	gcc Ala 420	aaa Lys	tca Ser	ggt Gly	ttg Leu	gcc Ala 425	gct Ala	tta Leu	atc Ile	acg Thr	gac Asp 430	gga Gly	ccc Pro	1296
Gly	Gly	Ser 435	Lys	Arg	atg Met	Tyr	Ala 440	Gly	Leu	Lys	Asn	Ala 445	Gly	Glu	Thr	1344
tgg Trp	tat Tyr 450	gac Asp	ata Ile	acg Thr	ggc Gly	aac Asn 455	cgt Arg	tca Ser	gat Asp	act Thr	gta Val 460	aaa Lys	atc Ile	gga Gly	tct Ser	1392
gac Asp 465	ggc Gly	tgg Trp	gga Gly	gag Glu	ttt Phe 470	cat His	gta Val	aac Asn	gat Asp	ggg Gly 475	tcc Ser	gtc Val	tcc Ser	att Ile	tat Tyr 480	1440
-	cag Gln	aaa Lys	taa													1452

<210> 14 <211> 483 <212> PRT

<213> Künstliche Sequenz

<223> Beschreibung der künstlichen Sequenz: Fusion der Alpha-Amylase-Gene von B. licheniformis und B. amyloliquefaciens (ALA34-84).

<400> 14 Val Asn Gly Thr Leu Met Gln Tyr Phe Glu Trp Tyr Thr Pro Asn Asp 10 Gly Gln His Trp Lys Arg Leu Gln Asn Asp Ala Glu His Leu Ser Asp 20 25 Ile Gly Ile Thr Ala Val Trp Ile Pro Pro Ala Tyr Lys Gly Thr Ser Gln Ala Asp Val Gly Tyr Gly Ala Tyr Asp Leu Tyr Asp Leu Gly Glu Phe His Gln Lys Gly Thr Val Arg Thr Lys Tyr Gly Thr Lys Gly Glu 75 Leu Gln Ser Ala Ile Gly Ser Leu His Ser Arg Asn Val Gln Val Tyr 90 Gly Asp Val Val Leu Asn His Lys Ala Gly Ala Asp Ala Thr Glu Asp 100 105 Val Thr Ala Val Glu Val Asn Pro Ala Asn Arg Asn Gln Glu Thr Ser 120 Glu Glu Tyr Gln Ile Lys Ala Trp Thr Asp Phe Arg Phe Pro Gly Arg 135 Gly Asn Thr Tyr Ser Asp Phe Lys Trp His Trp Tyr His Phe Asp Gly 150 155 Ala Asp Trp Asp Glu Ser Arg Lys Ile Ser Arg Ile Phe Lys Phe Arg 165 170 Gly Glu Gly Lys Ala Trp Asp Trp Glu Val Ser Ser Glu Asn Gly Asn 180 185 Tyr Asp Tyr Leu Met Tyr Ala Asp Val Asp Tyr Asp His Pro Asp Val 200 205 Val Ala Glu Thr Lys Lys Trp Gly Ile Trp Tyr Ala Asn Glu Leu Ser 215 220 Leu Asp Gly Phe Arg Ile Asp Ala Ala Lys His Ile Lys Phe Ser Phe 230 235 Leu Arg Asp Trp Val Gln Ala Val Arg Gln Ala Thr Gly Lys Glu Met 245 250 Phe Thr Val Ala Glu Tyr Trp Gln Asn Asn Ala Gly Lys Leu Glu Asn 265 270 Tyr Leu Asn Lys Thr Ser Phe Asn Gln Ser Val Phe Asp Val Pro Leu 280 His Phe Asn Leu Gln Ala Ala Ser Ser Gln Gly Gly Gly Tyr Asp Met 295 300 Arg Arg Leu Leu Asp Gly Thr Val Val Ser Arg His Pro Glu Lys Ala 310 315 Val Thr Phe Val Glu Asn His Asp Thr Gln Pro Gly Gln Ser Leu Glu 325 330 Ser Thr Val Gln Thr Trp Phe Lys Pro Leu Ala Tyr Ala Phe Ile Leu 345 Thr Arg Glu Ser Gly Tyr Pro Gln Val Phe Tyr Gly Asp Met Tyr Gly 360 Thr Lys Gly Thr Ser Pro Lys Glu Ile Pro Ser Leu Lys Asp Asn Ile 375 380 Glu Pro Ile Leu Lys Ala Arg Lys Glu Tyr Ala Tyr Gly Pro Gln His 390 395 Asp Tyr Ile Asp His Pro Asp Val Ile Gly Trp Thr Arg Glu Gly Asp 410 Ser Ser Ala Ala Lys Ser Gly Leu Ala Ala Leu Ile Thr Asp Gly Pro

420 425 430 Gly Gly Ser Lys Arg Met Tyr Ala Gly Leu Lys Asn Ala Gly Glu Thr 440 445 Trp Tyr Asp Ile Thr Gly Asn Arg Ser Asp Thr Val Lys Ile Gly Ser 455 460 Asp Gly Trp Gly Glu Phe His Val Asn Asp Gly Ser Val Ser Ile Tyr 470 475 Val Gln Lys <210> 15 <211> 1458 <212> DNA <213> Künstliche Sequenz <220> <223> Beschreibung der künstlichen Sequenz: Fusion der Alpha-Amylase-Gene von B. licheniformis und B. amyloliquefaciens (LAL19-433). <220> <221> CDS <222> (1)..(1458) <400> 15 gca aat ctt aat ggg acg ctg atg cag tat ttt gaa tgg tac atg ccc 48 Ala Asn Leu Asn Gly Thr Leu Met Gln Tyr Phe Glu Trp Tyr Met Pro aat gac ggc cag cat tgg aaa cga ttg cag aat gat gcg gaa cat tta 96 Asn Asp Gly Gln His Trp Lys Arg Leu Gln Asn Asp Ala Glu His Leu 20 teg gat ate gga ate act gee gte tgg att eet eee gea tae aaa gga Ser Asp Ile Gly Ile Thr Ala Val Trp Ile Pro Pro Ala Tyr Lys Gly 40 ttg agc caa tcc gat aac gga tac gga cct tat gat ttg tat gat tta 192 Leu Ser Gln Ser Asp Asn Gly Tyr Gly Pro Tyr Asp Leu Tyr Asp Leu 50 55 gga gaa ttc cag caa aaa ggg acg gtc aga acg aaa tac ggc aca aaa 240 Gly Glu Phe Gln Gln Lys Gly Thr Val Arg Thr Lys Tyr Gly Thr Lys 65 tca gag ctt caa gat gcg atc ggc tca ctg cat tcc cgg aac gtc caa 288 Ser Glu Leu Gln Asp Ala Ile Gly Ser Leu His Ser Arg Asn Val Gln 85 gta tac gga gat gtg gtt ttg aat cat aag gct ggt gct gat gca aca Val Tyr Gly Asp Val Val Leu Asn His Lys Ala Gly Ala Asp Ala Thr 100 gaa gat gta act gcc gtc gaa gtc aat ccg gcc aat aga aat cag gaa 384 Glu Asp Val Thr Ala Val Glu Val Asn Pro Ala Asn Arg Asn Gln Glu 115 120 125 act tcg gag gaa tat caa atc aaa gcg tgg acg gat ttt cgt ttt ccg

Thr	Ser 130	Glu	Glu	Tyr	Gln	Ile 135	Lys	Ala	Trp	Thr	<b>Asp</b> 140	Phe	Arg	Phe	Pro	
	cgt Arg			_		_	-									480
	gga Gly															528
	cgt Arg															576
	aac Asn															624
	gtc Val 210															672
	tca Ser															720
	ttt Phe															768
	atg Met															816
	aac Asn															864
	ctt Leu 290															912
	atg Met															960
	gcg Ala															1008
	gaa Glu															1056
	ttg Leu															1104

tac Tyr	999 Gly 370	aca Thr	aaa Lys	Gly	aca Thr	tcg Ser 375	cca Pro	aag Lys	gaa Glu	att Ile	Pro 380	tca Ser	ctg Leu	aaa Lys	gat Asp	1152
aat Asn 385	ata Ile	gag Glu	ccg Pro	att Ile	tta Leu 390	aaa Lys	gcg Ala	cgt Arg	aag Lys	gag Glu 395	tac Tyr	gca Ala	tac Tyr	Gly	ccc Pro 400	1200
cag Gln	cac His	gat Asp	tat Tyr	att Ile 405	gac Asp	cac His	ccg Pro	gat Asp	gtg Val 410	atc Ile	gga Gly	tgg Trp	acg Thr	agg Arg 415	gaa Glu	1248
ggt Gly	gac Asp	agc Ser	tcc Ser 420	gcc Ala	gcc Ala	aaa Lys	tca Ser	ggt Gly 425	ttg Leu	gcc Ala	gct Ala	tta Leu	atc Ile 430	acg Thr	gac Asp	1296
gga Gly	ccc Pro	ggt Gly 435	ggg Gly	gca Ala	aag Lys	cga Arg	atg Met 440	tat Tyr	gtc Val	ggc Gly	cgg Arg	caa Gln 445	aac Asn	gcc Ala	ggt Gly	1344
gag Glu	aca Thr 450	tgg Trp	cat His	gac Asp	att Ile	acc Thr 455	gga Gly	aac Asn	cgt Arg	tcg Ser	gag Glu 460	ccg Pro	gtt Val	gtc Val	atc Ile	1392
aat Asn 465	tcg Ser	gaa Glu	ggc Gly	tgg Trp	gga Gly 470	gag Glu	ttt Phe	cac His	gta Val	aac Asn 475	ggc Gly	Gly	tcg Ser	gtt Val	tca Ser 480	1440
	tat Tyr				tag											1458

<210> 16

<211> 485

<212> PRT

<213> Künstliche Sequenz

<223> Beschreibung der künstlichen Sequenz:Fusion der Alpha-Amylase-Gene von B. licheniformis und B. amyloliquefaciens (LAL19-433).

## <400> 16

Ala Asn Leu Asn Gly Thr Leu Met Gln Tyr Phe Glu Trp Tyr Met Pro 10 Asn Asp Gly Gln His Trp Lys Arg Leu Gln Asn Asp Ala Glu His Leu 20 25 Ser Asp Ile Gly Ile Thr Ala Val Trp Ile Pro Pro Ala Tyr Lys Gly 40 Leu Ser Gln Ser Asp Asn Gly Tyr Gly Pro Tyr Asp Leu Tyr Asp Leu 55 Gly Glu Phe Gln Gln Lys Gly Thr Val Arg Thr Lys Tyr Gly Thr Lys 70 75 Ser Glu Leu Gln Asp Ala Ile Gly Ser Leu His Ser Arg Asn Val Gln 85 90 Val Tyr Gly Asp Val Val Leu Asn His Lys Ala Gly Ala Asp Ala Thr 105 110 Glu Asp Val Thr Ala Val Glu Val Asn Pro Ala Asn Arg Asn Gln Glu 120 Thr Ser Glu Glu Tyr Gln Ile Lys Ala Trp Thr Asp Phe Arg Phe Pro

```
130
                         135
                                             140
Gly Arg Gly Asn Thr Tyr Ser Asp Phe Lys Trp His Trp Tyr His Phe
                    150
                                       155
Asp Gly Ala Asp Trp Asp Glu Ser Arg Lys Ile Ser Arg Ile Phe Lys
                165
                                    170
Phe Arg Gly Glu Gly Lys Ala Trp Asp Trp Glu Val Ser Ser Glu Asn
                                185
Gly Asn Tyr Asp Tyr Leu Met Tyr Ala Asp Val Asp Tyr Asp His Pro
        195
                            200
Asp Val Val Ala Glu Thr Lys Lys Trp Gly Ile Trp Tyr Ala Asn Glu
                        215
Leu Ser Leu Asp Gly Phe Arg Ile Asp Ala Ala Lys His Ile Lys Phe
                    230
                                        235
Ser Phe Leu Arg Asp Trp Val Gln Ala Val Arg Gln Ala Thr Gly Lys
                                   250
Glu Met Phe Thr Val Ala Glu Tyr Trp Gln Asn Asn Ala Gly Lys Leu
                               265
Glu Asn Tyr Leu Asn Lys Thr Ser Phe Asn Gln Ser Val Phe Asp Val
                            280
Pro Leu His Phe Asn Leu Gln Ala Ala Ser Ser Gln Gly Gly Tyr
                        295
Asp Met Arg Arg Leu Leu Asp Gly Thr Val Val Ser Arg His Pro Glu
                    310
                                        315
Lys Ala Val Thr Phe Val Glu Asn His Asp Thr Gln Pro Gly Gln Ser
                325
                                    330
Leu Glu Ser Thr Val Gln Thr Trp Phe Lys Pro Leu Ala Tyr Ala Phe
            340
                                345
                                                    350
Ile Leu Thr Arg Glu Ser Gly Tyr Pro Gln Val Phe Tyr Gly Asp Met
                            360
                                                365
Tyr Gly Thr Lys Gly Thr Ser Pro Lys Glu Ile Pro Ser Leu Lys Asp
                        375
                                            380
Asn Ile Glu Pro Ile Leu Lys Ala Arg Lys Glu Tyr Ala Tyr Gly Pro
                    390
                                        395
Gln His Asp Tyr Ile Asp His Pro Asp Val Ile Gly Trp Thr Arg Glu
                405
                                    410
Gly Asp Ser Ser Ala Ala Lys Ser Gly Leu Ala Ala Leu Ile Thr Asp
            420
                               425
Gly Pro Gly Gly Ala Lys Arg Met Tyr Val Gly Arg Gln Asn Ala Gly
       435
                           440
Glu Thr Trp His Asp Ile Thr Gly Asn Arg Ser Glu Pro Val Val Ile
                        455
Asn Ser Glu Gly Trp Gly Glu Phe His Val Asn Gly Gly Ser Val Ser
                    470
Ile Tyr Val Gln Arg
```

<sup>&</sup>lt;210> 17

<sup>&</sup>lt;211> 1452

<sup>&</sup>lt;212> DNA

<sup>&</sup>lt;213> Künstliche Sequenz

<sup>&</sup>lt;220>

<sup>&</sup>lt;223> Beschreibung der künstlichen Sequenz: Fusion der Alpha-Amylas -Gene von B. licheniformis und B. amyloliquefaciens (LAL19-153).

<221> CDS <222> (1)(1452) <400> 17																
gca Ala 1	Asn	ctt Leu	aat Asn	ggg Gly 5	Thr	ctg Leu	atg Met	cag Gln	tat Tyr 10	Phe	gaa Glu	tgg Trp	tac Tyr	atg Met 15	Pro	48
aat Asn	gac Asp	ggc	cag Gln 20	His	tgg Trp	aaa Lys	cga Arg	ttg Leu 25	cag Gln	aat Asn	gat Asp	gcg Ala	gaa Glu 30	cat His	tta Leu	96
tcg Ser	gat Asp	atc Ile 35	gga Gly	atc Ile	act Thr	gcc Ala	gtc Val 40	tgg Trp	att Ile	cct Pro	ccc Pro	gca Ala 45	tac Tyr	aaa Lys	gga Gly	144
ttg Leu	agc Ser 50	caa Gln	tcc Ser	gat Asp	aac Asn	gga Gly 55	tac Tyr	gga Gly	cct Pro	tat Tyr	gat Asp 60	Leu	tat Tyr	gat Asp	tta Leu	192
gga Gly 65	gaa Glu	ttc Phe	cag Gln	caa Gln	aaa Lys 70	GJĀ	acg Thr	gtc Val	aga Arg	acg Thr 75	aaa Lys	tac Tyr	ggc	aca Thr	aaa Lys 80	240
tca Ser	gag Glu	ctt Leu	caa Gln	gat Asp 85	gcg Ala	atc Ile	ggc	tca Ser	ctg Leu 90	cat His	tcc Ser	cgg Arg	aac Asn	gtc Val 95	caa Gln	288
gta Val	tac Tyr	gga Gly	gat Asp 100	gtg Val	gtt Val	ttg Leu	aat Asn	cat His 105	aag Lys	gct Ala	ggt Gly	gct Ala	gat Asp 110	gca Ala	aca Thr	336
gaa Glu	gat Asp	gta Val 115	act Thr	gcc Ala	gtc Val	gaa Glu	gtc Val 120	aat Asn	ccg Pro	gcc Ala	aat Asn	aga Arg 125	aat Asn	cag Gln	gaa Glu	384
act Thr	tcg Ser 130	gag Glu	gaa Glu	tat Tyr	caa Gln	atc Ile 135	aaa Lys	gcg Ala	tgg Trp	acg Thr	gat Asp 140	ttt Phe	cgt Arg	ttt Phe	ccg Pro	432
ggc Gly 145	cgt Arg	gga Gly	aac Asn	acg Thr	tac Tyr 150	agt Ser	gat Asp	ttt Phe	aaa Lys	tgg Trp 155	cat His	tgg Trp	tac Tyr	cat His	ttt Phe 160	480
gac Asp	gga Gly	acc Thr	gat Asp	tgg Trp 165	gac Asp	gag Glu	tcc Ser	cga Arg	aag Lys 170	ctg Leu	aac Asn	cgc Arg	atc Ile	tat Tyr 175	aag Lys	528
ttt Phe	caa Gln	gga Gly	aag Lys 180	gct Ala	tgg Trp	gat Asp	tgg Trp	gaa Glu 185	gtt Val	tcc Ser	aat Asn	gaa Glu	aac Asn 190	ggc Gly	aac Asn	576
tat Tyr	gat Asp	tat Tyr 195	ttg Leu	atg Met	tat Tyr	gcc Ala	gac Asp 200	atc Ile	gat Asp	tat Tyr	gac Asp	cat His 205	cct Pro	gat Asp	gtc Val	624
gca Ala	gca Ala 210	gaa Glu	att Ile	aag Lys	aga Arg	tgg Trp 215	ggc Gly	act Thr	tgg Trp	tat Tyr	gcc Ala 220	aat Asn	gaa Glu	ctg Leu	caa Gln	672

ttg Leu 225	gac Asp	ggt Gly	ttc Phe	cgt Arg	ctt Leu 230	Asp	gct Ala	gtc Val	aaa Lys	cac His 235	Ile	aaa Lys	ttt Phe	tct Ser	ttt Phe 240	720
ttg Leu	cgg Arg	gat Asp	tgg Trp	gtt Val 245	Asn	cat His	gtc Val	agg Arg	gaa Glu 250	Lys	acg Thr	Gly	aag Lys	gaa Glu 255	atg Met	768
ttt Phe	acg Thr	gta Val	gct Ala 260	Glu	tat Tyr	tgg Trp	cag Gln	aat Asn 265	gac Asp	ttg Leu	ggc Gly	gcg Ala	ctg Leu 270	gaa Glu	aac Asn	816
tat Tyr	ttg Leu	aac Asn 275	aaa Lys	aca Thr	aat Asn	ttt Phe	aat Asn 280	cat His	tca Ser	gtg Val	ttt Phe	gac Asp 285	gtg Val	ccg Pro	ctt Leu	864
cat His	tat Tyr 290	cag Gln	ttc Phe	cat His	gct Ala	gca Ala 295	tcg Ser	aca Thr	cag Gln	gga Gly	ggc Gly 300	ggc Gly	tat Tyr	gat Asp	atg Met	912
agg Arg 305	aaa Lys	ttg Leu	ctg Leu	aac Asn	agt Ser 310	acg Thr	gtc Val	gtt Val	tcc Ser	aag Lys 315	cat His	ccg Pro	ttg Leu	aaa Lys	gcg Ala 320	960
gtt Val	aca Thr	ttt Phe	gtc Val	gat Asp 325	aac Asn	cat His	gat Asp	aca Thr	cag Gln 330	ccg Pro	ggg Gly	caa Gln	tcg Ser	ctt Leu 335	gag Glu	1008
tcg Ser	act Thr	gtc Val	caa Gln 340	aca Thr	tgg Trp	ttt Phe	aag Lys	ccg Pro 345	ctt Leu	gct Ala	tac Tyr	gct Ala	ttt Phe 350	att Ile	ctc Leu	1056
aca Thr	agg Arg	gaa Glu 355	tct Ser	gga Gly	tac Tyr	cct Pro	cag Gln 360	gtt Val	ttc Phe	tac Tyr	Gly	gat Asp 365	atg Met	tac Tyr	ggg Gly	1104
acg Thr	aaa Lys 370	gga Gly	gac Asp	tcc Ser	cag Gln	cgc Arg 375	gaa Glu	att Ile	cct Pro	gcc Ala	ttg Leu 380	aaa Lys	cac His	aaa Lys	att Ile	1152
gaa Glu 385	ccg Pro	atc Ile	tta Leu	aaa Lys	gcg Ala 390	aga Arg	aaa Lys	cag Gln	tat Tyr	gcg Ala 395	tac Tyr	gga Gly	gca Ala	cag Gln	cat His 400	1200
gat Asp	tat Tyr	ttc Phe	gac Asp	cac His 405	cat His	gac Asp	att Ile	gtc Val	ggc Gly 410	tgg Trp	aca Thr	agg Arg	gaa Glu	ggc Gly 415	gac Asp	1248
agc Ser	tcg Ser	gtt Val	gca Ala 420	aat Asn	tca Ser	ggt Gly	ttg Leu	gcg Ala 425	gca Ala	tta Leu	ata Ile	aca Thr	gac Asp 430	gga Gly	ccc Pro	1296
ggt Gly	Gly	gca Ala 435	aag Lys	cga Arg	atg Met	tat Tyr	gtc Val 440	ggc Gly	cgg Arg	caa Gln	aac Asn	gcc Ala 445	ggt Gly	gag Glu	aca Thr	1344
tgg Trp	cat His	gac Asp	att Ile	acc Thr	gga Gly	aac Asn	cgt Arg	tcg Ser	gag Glu	ccg Pro	gtt Val	gtc Val	atc Ile	aat Asn	tcg Ser	1392

gaa ggc tgg gga gag ttt cac gta aac ggc ggg tcg gtt tca att tat Glu Gly Trp Gly Glu Phe His Val Asn Gly Gly Ser Val Ser Ile Tyr 475 470 475 480

gtt caa aga tag Val Gln Arg

<210> 18

<211> 483

<212> PRT

<213> Künstliche Sequenz

<223> Beschreibung der künstlichen Sequenz: Fusion der Alpha-Amylase-Gene von B. licheniformis und B. amyloliquefaciens (LAL19-153).

<400> 18 Ala Asn Leu Asn Gly Thr Leu Met Gln Tyr Phe Glu Trp Tyr Met Pro 10 Asn Asp Gly Gln His Trp Lys Arg Leu Gln Asn Asp Ala Glu His Leu 25 Ser Asp Ile Gly Ile Thr Ala Val Trp Ile Pro Pro Ala Tyr Lys Gly 40 Leu Ser Gln Ser Asp Asn Gly Tyr Gly Pro Tyr Asp Leu Tyr Asp Leu 55 Gly Glu Phe Gln Gln Lys Gly Thr Val Arg Thr Lys Tyr Gly Thr Lys 70 Ser Glu Leu Gln Asp Ala Ile Gly Ser Leu His Ser Arg Asn Val Gln 85 Val Tyr Gly Asp Val Val Leu Asn His Lys Ala Gly Ala Asp Ala Thr 100 105 110 Glu Asp Val Thr Ala Val Glu Val Asn Pro Ala Asn Arg Asn Gln Glu 120 125 Thr Ser Glu Glu Tyr Gln Ile Lys Ala Trp Thr Asp Phe Arg Phe Pro 135 140 Gly Arg Gly Asn Thr Tyr Ser Asp Phe Lys Trp His Trp Tyr His Phe 150 155 Asp Gly Thr Asp Trp Asp Glu Ser Arg Lys Leu Asn Arg Ile Tyr Lys 165 170 Phe Gln Gly Lys Ala Trp Asp Trp Glu Val Ser Asn Glu Asn Gly Asn 180 185 190 Tyr Asp Tyr Leu Met Tyr Ala Asp Ile Asp Tyr Asp His Pro Asp Val 195 200 Ala Ala Glu Ile Lys Arg Trp Gly Thr Trp Tyr Ala Asn Glu Leu Gln 215 220 Leu Asp Gly Phe Arg Leu Asp Ala Val Lys His Ile Lys Phe Ser Phe 230 235 Leu Arg Asp Trp Val Asn His Val Arg Glu Lys Thr Gly Lys Glu Met 245 250 Phe Thr Val Ala Glu Tyr Trp Gln Asn Asp Leu Gly Ala Leu Glu Asn 260 265 Tyr Leu Asn Lys Thr Asn Phe Asn His Ser Val Phe Asp Val Pro Leu 275 280 His Tyr Gln Phe His Ala Ala Ser Thr Gln Gly Gly Gly Tyr Asp Met 295 300 Arg Lys Leu Leu Asn Ser Thr Val Val Ser Lys His Pro Leu Lys Ala 310 315 320

				Asp 325					330					335	
			340	Thr				345					350		
		355		Gly			360					365		_	-
	370			Ser		375					380	_		-	
385				Lys	390					395					400
				His 405					410			_		415	-
			420	Asn				425					430	_	
		435		Arg			440					445	_		
	450			Thr		455					460				
Glu 465	Gly	Trp	Gly	Glu	Phe 470	His	Val	Asn	Gly	Gly 475	Ser	Val	Ser	Ile	Tyr 480
Val	Gln	Arg													